



## SEQUENCE LISTING

### (1) GENERAL INFORMATION

- (i) APPLICANT: Reiter, Robert  
Witte, Owen
- (ii) TITLE OF THE INVENTION: PSCA: Prostate Stem Cell Antigen
- (iii) NUMBER OF SEQUENCES: 7
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Mandel & Adriano  
(B) STREET: 35 N. Arroyo Parkway, Suite 60  
(C) CITY: Pasadena  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 91103
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 09/038,261  
(B) FILING DATE: 10-MAR-1998  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/814,279  
(B) FILING DATE: 10-MAR-1997
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Sarah B. Adriano  
(B) REGISTRATION NUMBER: 34,470  
(C) REFERENCE/DOCKET NUMBER: 30435.54USI2
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 626-395-7801  
(B) TELEFAX: 626-395-0694  
(C) TELEX:

### (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 998 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...998

(D) OTHER INFORMATION: Human PSCA nucleotide sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
AGGGAGAGGC AGTGACCATG AAGGCTGTGC TGCTTGCCCT GTTGATGGCA GGCTTGCCCC    60
TGCAGCCAGG CACTGCCCTG CTGTGCTACT CCTGCAAAGC CCAGGTGAGC AACGAGGACT    120
GCCTGCAGGT GGAGAACTGC ACCCAGCTGG GGGAGCAGTG CTGGACCGCG CGCATCCGCG    180
CAGTTGGCCT CCTGACCGTC ATCAGCAAAG GCTGCAGCTT GAACTGCGTG GATGACTCAC    240
AGGACTACTA CGTGGGCAAG AAGAACATCA CGTGTCTGTGA CACCGACTTG TGCAACGCCA    300
GCGGGGCCCC TGCCCTGCAG CCGGCTGCCG CCATCCTTGC GCTGCTCCCT GCACTCGGCC    360
TGCTGCTCTG GGGACCCGGC CAGCTATAGG CTCTGGGGGG CCCCCTGCA GCCCAGCTG    420
GGTGTGGTGC CCCAGGCCCT TGTGCCACTC CTCACAGAAC CTGGCCCAGT GGGAGCCTGT    480
CCTGGTTCCCT GAGGCACATC CTAACGCAAG TTTGACCATG TATGTTTGCA CCCCTTTTCC    540
CCNAACCCTG ACCTTCCCCT GGGCCTTTTC CAGGATTCCN ACCNGGCAGA TCAGTTTTAG    600
TGANACANAT CCGCNTGCAG ATGGCCCCCT CAACCNNTTN TGTTGNTGTT TCCATGGCCC    660
AGCATTTTCC ACCCTTAACC CTGTGTTTCA GCACTTNTTC CCCCAGGAAG CCTTCCCTGC    720
CCACCCCAT TATGAATTGA GCCAGGTTTG GTCCGTGGTG TCCCCCGCAC CCAGCAGGGG    780
ACAGGCAATC AGGAGGGCCC AGTAAAGGCT GAGATGAAGT GGAAGTGAAGT GAACTGGAGG    840
ACAAGAGTTG ACGTGAGTTC CTGGGAGTTT CCAGAGATGG GGCTGGAGG CCTGGAGGAA    900
GGGGCCAGGC CTCACATTTG TGGGNTCCC GAATGGCAGC CTGAGCACAG CGTAGGCCCT    960
TAATAAACAC CTGTTGGATA AGCCAAAAAA AAAAAAAA    998
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...123

(D) OTHER INFORMATION: Human PSCA amino acid sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Lys Ala Val Leu Leu Ala Leu Leu Met Ala Gly Leu Ala Leu Gln
 1           5           10           15
Pro Gly Thr Ala Leu Leu Cys Tyr Ser Cys Lys Ala Gln Val Ser Asn
          20           25           30
Glu Asp Cys Leu Gln Val Glu Asn Cys Thr Gln Leu Gly Glu Gln Cys
          35           40           45
Trp Thr Ala Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys
          50           55           60
Gly Cys Ser Leu Asn Cys Val Asp Asp Ser Gln Asp Tyr Tyr Val Gly
          65           70           75           80
Lys Lys Asn Ile Thr Cys Cys Asp Thr Asp Leu Cys Asn Ala Ser Gly
          85           90           95
Ala His Ala Leu Gln Pro Ala Ala Ala Ile Leu Ala Leu Leu Pro Ala
          100          105          110
```

Leu Gly Leu Leu Leu Trp Gly Pro Gly Gln Leu  
115 120

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Other  
(B) LOCATION: 1...441  
(D) OTHER INFORMATION: mPSCA nucleotide sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGAAGACAG	TTTTTTTTTAT	CCTGCTGGCC	ACCTACTTAG	CCCTGCATCC	AGGTGCTGCT	60
CTGCAGTGCT	ATTCATGCAC	AGCACAGATG	AACAACAGAG	ACTGTCTGAA	TGTACAGAAC	120
TGCAGCCTGG	ACCAGCACAG	TTGCTTTTACA	TCGCGCATCC	GGGCCATTGG	ACTCGTGACA	180
GTTATCAGTA	AGGGCTGCAG	CTCACAGTGT	GAGGATGACT	CGGAGAACTA	CTATTTGGGC	240
AAGAAGAAACA	TCACGTGCTG	CTACTCTGAC	CTGTGCAATG	TCAACGGGGC	CCACACCCTG	300
AAGCCACCCA	CCACCCTGGG	GCTGCTGACC	GTGCTCTGCA	GCCTGTTGCT	GTGGGGCTCC	360
AGCCGTCTGT	AGGCTCTGGG	AGAGCCTACC	ATAGCCCGAT	TGTGAAGGGA	TGAGCTGCAC	420
TCCACCCAC	CCCCACACAG	G				441

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ix) FEATURE:

- (A) NAME/KEY: Other  
(B) LOCATION: 1...123  
(D) OTHER INFORMATION: mPSCA amino acid translation

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Lys	Thr	Val	Phe	Phe	Ile	Leu	Leu	Ala	Thr	Tyr	Leu	Ala	Leu	His
1				5					10					15	
Pro	Gly	Ala	Ala	Leu	Gln	Cys	Tyr	Ser	Cys	Thr	Ala	Gln	Met	Asn	Asn
			20					25					30		
Arg	Asp	Cys	Leu	Asn	Val	Gln	Asn	Cys	Ser	Leu	Asp	Gln	His	Ser	Cys
		35					40					45			
Phe	Thr	Ser	Arg	Ile	Arg	Ala	Ile	Gly	Leu	Val	Thr	Val	Ile	Ser	Lys
	50					55					60				
Gly	Cys	Ser	Ser	Gln	Cys	Glu	Asp	Asp	Ser	Glu	Asn	Tyr	Tyr	Leu	Gly
65					70					75				80	
Lys	Lys	Asn	Ile	Thr	Cys	Cys	Tyr	Ser	Asp	Leu	Cys	Asn	Val	Asn	Gly
				85					90					95	
Ala	His	Thr	Leu	Lys	Pro	Pro	Thr	Thr	Leu	Gly	Leu	Leu	Thr	Val	Leu
			100					105					110		

Cys Ser Leu Leu Leu Trp Gly Ser Ser Arg Leu  
115 120

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Lys	Ile	Phe	Leu	Pro	Val	Leu	Leu	Ala	Ala	Leu	Leu	Gly	Val	Glu
1				5					10					15	
Arg	Ala	Ser	Ser	Leu	Met	Cys	Phe	Ser	Cys	Leu	Asn	Gln	Lys	Ser	Asn
			20					25					30		
Leu	Tyr	Cys	Leu	Lys	Pro	Thr	Ile	Cys	Ser	Asp	Gln	Asp	Asn	Tyr	Cys
		35				40						45			
Val	Thr	Val	Ser	Ala	Ser	Ala	Gly	Ile	Gly	Asn	Leu	Val	Thr	Phe	Gly
	50					55				60					
His	Ser	Leu	Ser	Lys	Thr	Cys	Ser	Pro	Ala	Cys	Pro	Ile	Pro	Glu	Gly
65					70					75					80
Val	Asn	Val	Gly	Val	Ala	Ser	Met	Gly	Ile	Ser	Cys	Cys	Gln	Ser	Phe
				85					90					95	
Leu	Cys	Asn	Phe	Ser	Ala	Ala	Asp	Gly	Gly	Leu	Arg	Ala	Ser	Val	Thr
			100					105					110		
Leu	Leu	Gly	Ala	Gly	Leu	Leu	Leu	Ser	Leu	Leu	Pro	Ala	Leu	Leu	Arg
		115					120					125			
Phe	Gly	Pro	Leu	Leu	Leu	Trp	Gly	Pro	Gly	Gln	Leu				
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Lys	Ala	Val	Leu	Leu	Ala	Leu	Leu	Met	Ala	Gly	Leu	Ala	Leu	Gln
1				5					10					15	
Pro	Gly	Thr	Ala	Leu	Leu	Cys	Tyr	Ser	Cys	Lys	Ala	Gln	Val	Ser	Asn
			20					25					30		
Glu	Asp	Cys	Leu	Gln	Val	Glu	Asn	Cys	Thr	Gln	Leu	Gly	Glu	Gln	Cys
		35				40						45			
Trp	Thr	Ala	Arg	Ile	Arg	Ala	Val	Gly	Leu	Leu	Thr	Val	Ile	Ser	Lys
	50					55					60				
Gly	Cys	Ser	Leu	Asn	Cys	Val	Asp	Asp	Ser	Gln	Asp	Tyr	Tyr	Val	Gly
65				70					75						80
Lys	Lys	Asn	Ile	Thr	Cys	Cys	Asp	Thr	Asp	Leu	Cys	Asn	Ala	Ser	Gly
			85						90					95	
Ala	His	Ala	Leu	Gln	Pro	Ala	Ala	Ala	Ile	Leu	Ala	Leu	Leu	Pro	Ala
			100					105					110		

Leu Gly Leu Leu Leu Trp Gly Pro Gly Gln Leu  
115 120

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Lys Thr Val Leu Phe Leu Leu Leu Ala Thr Tyr Leu Ala Leu His  
1 5 10 15  
Pro Gly Ala Ala Leu Gln Cys Tyr Ser Cys Thr Ala Gln Met Asn Asn  
20 25 30  
Arg Asp Cys Leu Asn Val Gln Asn Cys Ser Leu Asp Gln His Ser Cys  
35 40 45  
Phe Thr Ser Arg Ile Arg Ala Ile Gly Leu Val Thr Val Ile Ser Lys  
50 55 60  
Gly Cys Ser Ser Gln Cys Glu Asp Asp Ser Glu Asn Tyr Tyr Leu Gly  
65 70 75 80  
Lys Lys Asn Ile Thr Cys Cys Tyr Ser Asp Leu Cys Asn Val Asn Gly  
85 90 95  
Ala His Thr Leu Lys Pro Pro Thr Thr Leu Gly Leu Leu Thr Val Leu  
100 105 110  
Cys Ser Leu Leu Leu Trp Gly Ser Ser Arg Leu  
115 120